```
  1  GTCGACCCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGG
     CAGCTGGGTGCGCAGGCCGTCGTCCGTCCGACGTCGTCCGCTCGTCGTCGTTCTCATTTTCC

 63  TGACCGCGGCTGCCCACCCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTT
     ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCCGTGCTCTACGGTAGGACCTGCGAGAA
                             1▶ M  G  R  A  R  D  A  I  L  D  A  L

125  GAAAACTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
     CTTTTGAACAGTCCCCTACTTGAGTTTTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC
     13▶ E  N  L  S  G  D  E  L  K  K  F  K  M  K  L  L  T  V  Q  L  R

187  AGAAGGCTATGGGCGCATCCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
     TCTTCCGATACCCGCGTAGGGTGCGCCCCGGGACGACGTCTACCTGCGGTATCTAGAGTGAC
     33▶ E  G  Y  G  R  I  P  R  G  A  L  L  Q  M  D  A  I  D  L  T

249  ACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCACAATGACTGTGCTTAGA
     TGTTTGAACAGTCGATGATAGACCTCAGCATACCGAACCTCGAGTGTTACTGACACGAATCT
     54▶ D  K  L  V  S  Y  Y  L  E  S  Y  G  L  E  L  T  M  T  V  L  R

311  GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
     CTGTACCCGAATGTCCTCGACCGACTCGTCGACGTTTGCTGATTTCTTCTCAGACCTCGACA
     75▶ D  M  G  L  Q  E  L  A  E  Q  L  Q  T  T  K  E  E  S  G  A  V

373  GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTGTGGACCAGC
     .CCGTCGACGTCGGTCACAGGGACGAGTCTCATGTCGGTCTTGTCCTGTGAAACACCTGGTCG
     95▶ A  A  A  A  S  V  P  A  Q  S  T  A  R  T  G  H  F  V  D  Q

435  ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGCTGGATGCTTTGCATGGC
     TGTCCGTTCGTGAGTAACGGTCCCAGTGTCTTCACCTGCCTCACGACCTACGAAACGTACCG
     116▶H  R  Q  A  L  I  A  R  V  T  E  V  D  G  V  L  D  A  L  H  G

497  AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGACCACCAGCCAAGACAAGAT
     TCACACGACTGACTTCCTGTCATGGTCCGTCAAGCACGTCTCTGGTGGTCGGTTCTGTTCTA
     137▶S  V  L  T  E  G  Q  Y  Q  A  V  R  A  E  T  T  S  Q  D  K  M

559  GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
     CTCCTTCGAGAAGTCGAAACAAGGTAGGACCTTGGACTGGACGTTCCTGAGGGAGGAGGTCC
     157▶R  K  L  F  S  F  V  P  S  W  N  L  T  C  K  D  S  L  L  Q

621  CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
     GGAACTTCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG (SEQ ID NO:3)
     178▶A  L  K  E  I  H  P  Y  L  V  M  D  L  E  Q  S (SEQ ID NO:2)

683  AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTTGAAAAAACAATTTGTATTTGT
     TCGATGTAATAGATCGAGGACTGAAACATATGTGTTAAAAACTTTTTTGTTAAACATAAACA

745  GTTTAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC (SEQ ID NO:1)
     CAAATTTTTTTTTTTTTTTTTTTTTTTTCCCGCCGGCG
```

FIG. 1
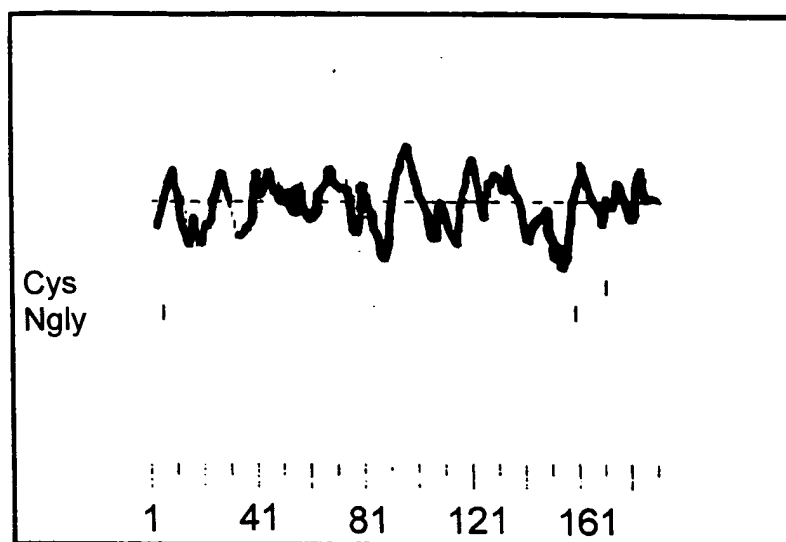
FIG. 2
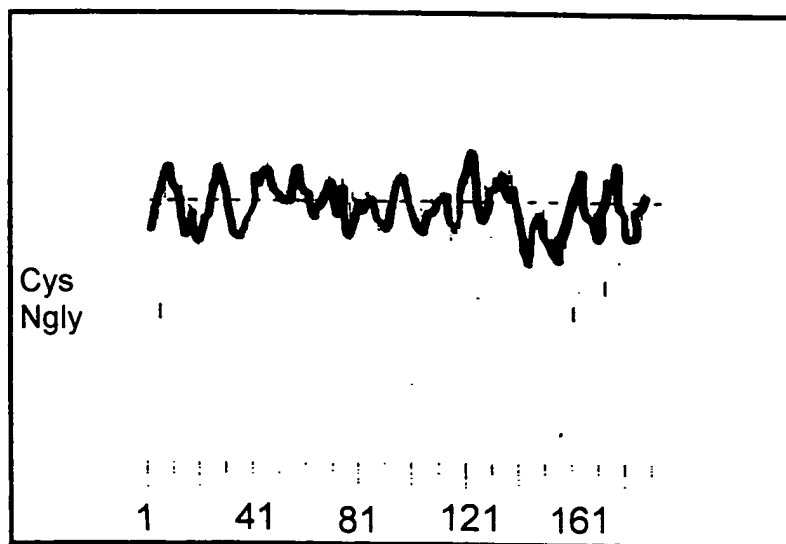
FIG. 4

```
  1  CGCGTCCGGCTGCAGCGGGGTGAGCGGCGGCAGCGGCCGGGGATCCTGGAGCCATGGGGC
     GCGCAGGCCGACGTCGCCCCACTCGCCGCCGTCGCCGGCCCCTAGGACCTCGGTACCCCG
                                                           1▶ M  G
```

```
 61  GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
     CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA
  3▶ R  A  R  D  A  I  L  D  A  L  E  N  L  T  A  E  E  L  K  K
```

```
121  TCAAGCTGAAGCTGCTGTCGGTGCCGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG
     AGTTCGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCGCGTAGGGCGCCCCGC
 23▶ F  K  L  K  L  L  S  V  P  L  R  E  G  Y  G  R  I  P  R  G
```

```
181  CGCTGCTGTCCATGGACGCCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
     GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTCGACCAGTCGAAGATGGACCTCT
 43▶ A  L  L  S  M  D  A  L  D  L  T  D  K  L  V  S  F  Y  L  E
```

```
241  CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCG
     GGATGCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGGACGTCCTCTACCGGC
 63▶ T  Y  G  A  E  L  T  A  N  V  L  R  D  M  G  L  Q  E  M  A
```

```
301  GGCAGCTGCAGGCGGCCACGCACCAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
     CCGTCGACGTCCGCCGGTGCGTGGTCCCGAGACCTCGGCGCGGTCGACCCTAGGTCCGGG
 83▶ G  Q  L  Q  A  A  T  H  Q  G  S  G  A · A  P · A  G  I  Q  A
```

```
361  CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
     GAGGAGTCAGCCGTCGGTTCGGTCCGGACGTGAAATATCTGGTCGTGGCCCGACGCGAAT
103▶ P  P  Q  S  A  A  K  P  G  L  H  F  I  D  Q  H  R  A  A  L
```

```
421  TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCCTGACGG
     AGCGCTCCCAGTGTTTGCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC
123▶ I  A  R  V  T  N  V  E  W  L  L  D  A  L  Y  G  K  V  L  T
```

```
481  ATGAGCAGTACCAGGCAGTGCGGGCCGAGCCCACCAACCCAAGCAAGATGCGGAAGCTCT
     TACTCGTCATGGTCCGTCACGCCCGGCTCGGGTGGTTGGGTTCGTTCTACGCCTTCGAGA
143▶ D  E  Q  Y  Q  A  V  R  A  E  P  T  N  P  S  K  M  R  K  L
```

```
541  TCAGTTTCACACCAGCCTGGAACTGGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
     AGTCAAAGTGTGGTCGGACCTTGACCTGGACGTTCCTGAACGAGGAGGTCCGGGATTCCC
163▶ F  S  F  T · P  A  W  N  W  T  C  K  D  L  L  L  Q  A  L  R
```

```
601  AGTCCCAGTCCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCCAGCAACAC
     TCAGGGTCAGGATGGACCACCTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG (SEQ ID NO:6)
183▶ E  S  Q  S  Y  L  V  E  D  L  E  R  S (SEQ ID NO:5)
```

```
661  TCCGGTCAGCCCCTGGCAATCCCACCAAATCATCCTGAATCTGATCTTTTTATACACAAT
     AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA
```

```
721  ATACGAAAAGCCAGCTTGAA (SEQ ID NO:4)
     TATGCTTTTCGGTCGAACTT
```

FIG. 3

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hCARD5-DNA                                      740 aa vs.
> mCARD5-DNA                                      763 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
68.2% identity;    Global alignment score: 2377


               10        20        30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC------------GGC
       :    :::::::::::.::: :.:: ::    .::: ::.:.::::             :.:
       CCACGCGTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGGTGAC
           10        20        30        40        50        60


        40        50        60        70        80        90
inputs CGGGGAT------CCTGGAGCCATGGGGCGCGCGCGCGACGCCATCCTGGATGCGCTGGA
       :: :: :         :: .:::::::::::::: ::.:: :: :::::::::::: :: :: ::
       CGCGGCTGCCCACCCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTTGA
           70        80        90       100       110       120


       100       110       120       130       140       150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCG
       .::: ::.:  :    ::  ::.:::::::.::::::::: :::::::::::::::.:.:::: .::::::
       AAACTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
           130       140       150       160       170       180


       160       170       180       190       200       210
inputs CGAGGGCTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
       ::.:::::: :::::::::::::.:: :: :: ::::::    :::::::::::.:.::: :::::
       AGAAGGCTATGGGCGCATCCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
           190       200       210       220       230       240


       220       230       240       250       260       270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCGCTAAC-GTGC
       :::::::.:: :::::::::.:::: :::::::.: :: ::: :::::::::: . :.:: ::::
       TGACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
           250       260       270       280       290


       280       290       300       310       320       330
inputs TGCGCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
       :   : :::::::::: :.::::::: :::: :.::::::::::.: :   . : ::.: :
       TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
     300       310       320       330       340       350


       340       350       360       370       380       390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
       :::::::: : : :::::::: .. : . : :::: :::::. .:::::::.. :::: .:
       CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
         360       370       380       390       400       410


       400       410       420       430       440       450
```

<p align="center">FIG. 5A</p>

```
inputs  ACTTTATAGACCAGCACCGGGCTGCGCTTATCGCGAGGGTCACAAACGTTGAGTGGCTGC
        ::::::.:.::::::::::: ::  .::.:: :: :: ::::::::::.: :: ::  :. :::
        ACTTTGTGGACCAGCACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGC
           420       430       440       450       460       470


                460       470       480       490       500       510
inputs  TGGATGCTCTGTACGGGAAGGTCCTGACGGATGAGCAGTACCAGGCAGTGCGGGCCGAGC
        :::::::: :: : :: :. :: ::::: ::..:..::::::::::::::: :: :: :::
        TGGATGCTTTGCATGGCAGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGA
           480       490       500       510       520       530


                520       530       540       550       560       570
inputs  CCACCAACCCAAGCAAGATGCGGAAGCTCTTCAGTTTCACACCAGCCTGGAACTGGACCT
        ::::::.:: :..:::::::: ::::::::::::: :: . ..::: :::::::: :::::
        CCACCAGCCAAGACAAGATGAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCT
           540       550       560       570       580       590


                580       590       600       610       620       630
inputs  GCAAGGACTTGCTCCTCCAGGCCCTAAGGGAGTCCCAGTCCTACCTGGTGGAGGACCTGG
        :::::::::  :::::::::::: :.:.::.. :: ::::: :::::..::::::::::
        GCAAGGACTCCCTCCTCCAGGCCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGG
           600       610       620       630       640       650


                640       650       660       670       680
inputs  AGCGGAGCTGAGGC-TCCTTCCCAGCAACACTCCGGTC-AGCCCCTGGCAAT-CCCAC-C
        :::.:::::::::: :: :: :::::.::: :  .:: ::: ::::.:..:  :: :
        AGCAGAGCTGAGGTATCTTTTCCAGCTACATT---ATCTAGCTCCTGACTTTGTATACAC
           660       670       680       690       700       710


          690       700       710       720       730       740
inputs  AAATCATCCTGAATCTGATCTTTTTATACACAATATACGAAAAGCCAGCTTGAA (SEQ ID NO:4)
        ::.: .:  ..::.:...: : :.::. .  ...:: .:::::.  :. .....:
        AATTTTTGAAAAAACAATT-TGTATTTGTGTTTAAAAAAAAAAAAAAAAAAAGG (SEQ ID NO:1)
           720       730       740       750       760
```

FIG. 5B

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hCARD5-protein                                    195 aa vs.
> mCARD5-protein                                    193 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
71.8% identity;   Global alignment score: 712


              10        20        30        40        50        60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
       :::::::::::::::...::::::.:::.:.:::::::::::::: :::.:::::::::.:
       MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSYY
              10        20        30        40        50        60


              70        80        90       100       110       120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
       ::.:: :::  .:::::::::.: :::. : .  :::...:   .:.::.:. : ::.::::
       LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
              70        80        90       100       110


             130       140       150       160       170       180
inputs ALIARVTNVEWLLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
       :::::::::.:.  ..:::: : :::.  ::::::::: :....:::::::::.:.:: :::: ::::
       ALIARVTEVDGVLDALHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTCKDSLLQA
      120       130       140       150       160       170


             190
inputs LRESQSYLVEDLERS  (SEQ ID NO:5)
       :.:  ..:::  ::::.:
       LKEIHPYLVMDLEQS  (SEQ ID NO:2)
      180       190
```
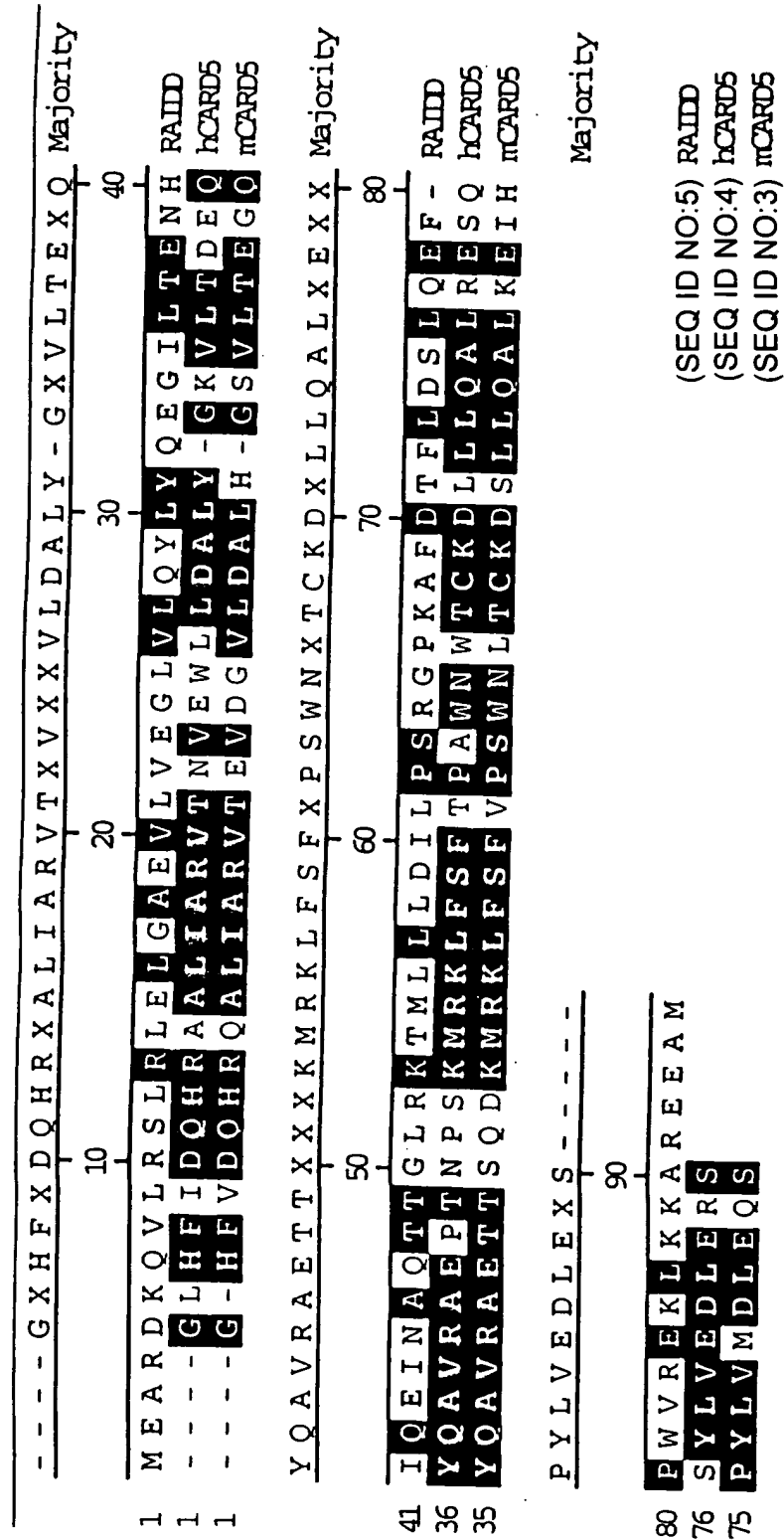
FIG. 6

Applicant(s): John Bertin
NOVEL MOLECULES OF THE CARD-RELATED PROTEIN
FAMILY AND USES THEREOF

```
              10        20        30        40
Majority  ---GXHFXDQHRXALIARVTXVXXVLDALY-GXVLTEXQ

1  MEARDKQVLRSLRLELGAEVLVEGLVLQYLYQEGILTENH  RAIDD
1  ---GLHFIDQHRAALIARVTNVEWLLDALY-GKVLTDEQ  hCARD5
1  ---GHFVDQHRQALIARVTEVDGVLDALH-GSVLTEGQ   mCARD5

              50        60        70        80
Majority  YQAVRAETTXXXKMRKLFSFXPSWNXTCKDXLLQALXEXX

41 IQEINAQTTGLRKTMLLLDILPSRGPKAFDTFLDSLQEF-  RAIDD
36 YQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQALRESQ  hCARD5
35 YQAVRAETTSQDKMRKLFSFVPSWNLTCKDSLLQALKEIH  mCARD5

              90
Majority  PYLVEDLEXS-----

80 PWREKLKKAREEAM   RAIDD
76 SYLVEDLERS       hCARD5
75 PYLVMDLEQS       mCARD5
```

(SEQ ID NO:5) RAIDD
(SEQ ID NO:4) hCARD5
(SEQ ID NO:3) mCARD5

FIG. 7

FIG. 8